In the Specification

Please replace the paragraph beginning on page 51, line 15 with the following:

The primary goal of the design process is the creation of groups of primer pairs with a common annealing temperature (T_m). When the program could identify a primer pair for any gene that fit the criteria, the gene is removed from the bin of genes needing primer design. Genes remaining in the bin are subjected to additional rounds of primer-picking, with the gradual and simultaneous relaxation of the criteria (*i.e.*, lowering the annealing temperature, increasing the size of the window where primers could be predicted, expanding the range of permitted size and G+C content, removing the need for a G/C clamp), until primers are picked for about 8,000 of the about 12,000 ENUs of this invention. After the *E. nidulans* specific portion of the primers is selected, an additional common primer tail sequence (universal primer) is added to the 5' ends. For the forward primers, the additional common bases added are: (5'-GAATTCACTGCGGCCGCCATG-3', SEQ ID NO: 44346); for the reverse primers the additional common bases added are: (5'-GTTCTCGAGACGAGCGATCGC-3', SEQ ID NO: 44347). The universal primer tail sequences are added so that subsequent reamplifications of any primer pair can be done with a single set of primers. In addition, the primer tail sequences contain restriction digestion sites for 8 bp cutters (NotI and SgfI) and 6 bp cutters (EcoRI and XhoI) to facilitate cloning of ENUs into vectors. The forward primers contains EcoRI and NotI restriction sites; the reverse primers contains XhoI and SgfI restriction sites.